

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2003, 15:20:58 ; Search time 2393 Seconds
(without alignments)
15773.026 Million cell updates/sec

Title: US-09-745-506-74

Perfect score: 1553
Sequence: 1 GTGATGTTATCTTGTCGTCTTCTGTTTACTTAACATTCAA 1553

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 22781392 segs, 12152238056 residues

Word size: 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

EST: *
1: em_estbda: *
2: em_esthum: *
3: em_estlin: *
4: em_estnu: *
5: em_estrov: *
6: em_estrpl: *
7: em_estro: *
8: em_estrl: *
9: gb_est1: *
10: gb_est2: *
11: gb_est3: *
12: gb_est4: *
13: gb_est5: *
14: gb_estfun: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vit: *
21: em_gss_fun: *
22: em_gss_man: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rtd: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	858	55.2	930 13 BX393871	BX393871 BX393871
2	833	53.6	857 13 B0172435	B0172435 AGENCOURT
3	827	53.3	1201 9 AL581997	AL581997 AL581997
4	808	52.0	1201 13 BX446370	BX446370 BX446370

	5	787	50.7	957	9	AL521920	AL521920
	6	784	50.5	1117	12	BM545164	BM545164 AGENCOURT
	7	769	49.5	836	13	B0229243	B0229243 AGENCOURT
	8	763	49.1	1201	9	AL529615	AL529615
	9	732	47.1	1019	13	B0859307	B0859307 AGENCOURT
	10	722	46.5	1019	12	BM557530	BM557530 AGENCOURT
	11	720	46.4	890	9	AL520538	AL520538
	12	677	43.6	759	13	BE275324	BE275324 601122173
	13	675	43.5	919	13	B0526538	B0526538 AGENCOURT
	14	674	43.4	877	13	B0437698	B0437698 AGENCOURT
	15	652	42.0	963	10	BE797115	BE797115 601587094
	16	646	41.6	909	14	CD385139	CD385139 AGENCOURT
	17	640	41.2	728	14	CD102399	CD102399 AGENCOURT
	18	627	40.4	762	12	BG762023	BG762023 602718981
	19	626	40.3	1031	13	BX385102	BX385102
	20	622	40.1	742	12	B1093955	B1093955 602857854
	21	611	39.3	817	12	B1755123	B1755123 603022837
	22	609	39.2	859	10	BE797593	BE797593 602246134
	23	609	39.0	888	13	B0195469	B0195469 AGENCOURT
	24	605	38.5	945	10	BE747311	BE747311 601580280
	25	598	38.5	909	13	B0165031	B0165031 AGENCOURT
	26	594	38.2	958	10	BE973889	BE973889 602242014
	27	593	38.2	845	10	BG754550	BG754550 602710167
	28	592	38.1	985	13	BQ927763	BQ927763 AGENCOURT
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	31	581	37.4	980	13	B0854847	B0854847 AGENCOURT
	32	574	37.0	666	13	B0663511	B0663511 61102603
	33	569	36.6	807	12	B1766329	B1766329 603052429
	34	568	36.6	568	14	CB122465	CB122465 K-EST0170
	35	568	36.6	732	10	BG472953	BG472953 602514888
	36	567	36.5	796	9	AU134237	AU134237
	37	566	36.4	638	14	CB122989	CB122989 K-EST0171
	38	563	36.3	1119	10	BG745052	BG745052 602723147
	39	559	36.0	610	12	BM841141	BM841141 K-EST0118
	40	557	35.9	600	14	CB146277	CB146277 K-EST0201
	41	555	35.7	1201	9	AL523986	AL523986
	42	549	35.4	549	12	BM712181	BM712181 UI-E-DW1
	43	549	35.4	871	12	BG765986	BG765986 602738046
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	45	546	35.2	753	10	AM957667	AM957667 EST369737

ALIGNMENTS

RESULT 1
LOCUS BX393871
DEFINITION BX393871 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DC005YM21 5-PRIME, mRNA sequence.

ACCESSION BX393871
VERSION BX393871.1
KEYWORDS GI:30624084
SOURCE EST.

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 930)
AUTHORS Li, M.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length CDNA libraries and normalization
JOURNAL Unpublished

COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0DC005AG101P1cluster-1287.f. Contact :
Feng Liang Email: fliang@litech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600

FEATURES Faraday Avenue Genoscope sequence ID : CS0DC005AG110P1.
Location/Qualifiers
Source 1..930
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC005YM21"
/issue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 248 a 231 c 214 g 237 t

Query Match 55.2%; Score 858; DB 13; Length 930;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 858; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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73 GTCCCGACGACAGTCCGGTTTGTAGATTCCTGATTCGAATTCCTCCGTTCTTCATG 132
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248 GATTGAAGGCTCTCTTCTTCTTCTTGAATGACTTTCATCCCTCTGTTGCTGAGAGT 307
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133 GATTGAAGGCTCTCTTCTTCTTCTTGAATGACTTTCATCCCTCTGTTGCTGAGAGT 192
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308 TGGGACATGTGGATTAATGATGGAACCAAGCCACACATCTGTAATATACATCTTC 367
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193 TGGGACATGTGGATTAATGATGGAACCAAGCCACACATCTGTAATATACATCTTC 252
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368 CTGACCAATGACCTGACTGAGGAAGATGATGAGAGAGTCTGCMAAAGAGCAGACCTC 427
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253 CTGACCAATGACCTGACTGAGGAAGATGATGAGAGAGTCTGCMAAAGAGCAGACCTC 312
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428 ATTCTCTCTACACCGGCTATCTTCCACCCATTAAGGCTAATCTGAGACATATG 487
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313 ATTCTCTCTACACCGGCTATCTTCCGACCCATTAAGGCTAATCTGAGACATATG 372
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488 AAGGAGCGCTGTGTATCGGGCTGTGGAACAGAGTGGTATCTACTCTCTCTACATA 547
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373 AAGGAGCGCTGTGTATCGGGCTGTGGAACAGAGTGGTATCTACTCTCTCTACATA 432
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548 GCGTATGATGTGCGGCCAGGGCGTCAACACTGTGGCTTAAGGGCTTGGAGCTTGT 607
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433 GCGTATGATGTGCGGCCAGGGCGTCAACACTGTGGCTTAAGGGCTTGGAGCTTGT 492
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608 ACCTCAGGCGCTATATCTTCCCAAGCTCCCACTACCTCAAGAGGAAACCAACCGA 667
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493 ACCTCAGGCGCTATATCTTCCCAAGCTCCCACTACCTCAAGAGGAAACCAACCGA 552
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668 GTGAATTCACGTTAATACCAACCAAGCTGAGCAAAAGTCTGCTGAGTGAAGA 727
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728 ATTGACGGTGTCTGTCACTTCTTCTTCTGCTAGAGCTGTGTAAGAGAACAACAGG 787
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613 ATTGACGGTGTCTGTCACTTCTTCTTCTGCTAGAGCTGTGTAAGAGAACAACAGG 672
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788 ATTAATCTGAATGTCTCAGAAAGGTTGATGAGAGTGGTATATTTCTTCCCGGAAC 847
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673 ATTAATCTGAATGTCTCAGAAAGGTTGATGAGAGTGGTATATTTCTTCCCGGAAC 732
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848 AAACAACCTTATCAGAGAGCAAAATCTGTCACTGAGAGAGCTTGTGCTTACATAT 907
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733 AAACAACCTTATCAGAGAGCAAAATCTGTCACTGAGAGAGCTTGTGCTTACATAT 792
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908 GGAATGGAGAGGTTATGACACACTGATGATCTGTCTCCCTGGCAACATGATGATGCA 967
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793 GGAATGGAGAGGTTATGACACACTGATGATCTGTCTCCCTGGCAACATGATGATGCA 852
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968 ATTAAGAGACACCTAAACATATCTCATATTCGCTTAGCCCTGGGGTGGGAGAACCTTA 1027
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Db 853 ATTAAGAGACACCTAAACATATCTCATATTCGCTTAGCCCTTGGGGTGGGAGAACCTTA 912
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QY 1028 GAGTCTCAAGTCAAACTC 1045
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Db 913 GAGTCTCAAGTCAAACTC 930
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RESULT 2
BU172435 857 bp mRNA linear EST 04-SEP-2002
LOCUS AGENCOURT_7970438 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6164871
DEFINITION 5', mRNA sequence.
ACCESSION BU172435
VERSION BU172435.1 GI:22686419
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 857)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCPD/DPF
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM13522 row: k column: 16
High quality sequence stop: 728.

FEATURES Location/Qualifiers
Source 1..857
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6164871"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 234 a 201 c 199 g 223 t

Query Match 53.6%; Score 833; DB 13; Length 857;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 833; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

492 AGCGCCTGTGTATCCGGCTCTGAGAACAGATCGGTATCTCTCTCATACAGCT 551
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1 AGCGCCTGTGTATCCGGCTCTGAGAACAGATCGGTATCTCTCTCATACAGCT 60
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552 ATGATGCTGGGCCCGCCAGGGGCTCAACACTGGTTGGCTAAAGGCTTGAAGCTTGAACCT 611
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61 ATGATGCTGGGCCCGCCAGGGGCTCAACACTGGTTGGCTAAAGGCTTGAAGCTTGAACCT 120
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612 CCAGGCCCATATCTCTCCAAAGCTCCCACTACCTCAAGAGGAAACCAACGAGTAG 671
|||||
121 CCAGGCCCATATCTCTCCAAAGCTCCCACTACCTCAAGAGGAAACCAACGAGTAG 180
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672 AATTCAAGCTTAACACCAACCAAGCTGAGCAAAAGTCAATGTCTGCAAGTGAAGTAATG 731
|||||
181 AATTCAAGCTTAACACCAACCAAGCTGAGCAAAAGTCAATGTCTGCAAGTGAAGTAATG 240
|||||
732 ACGGTGTTCTGTCACTTCTTCTTCTGCTAGAGCTGTATGAGAACCAACGAGTATTA 791
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Db 241 ACGGTGTTTCTGTCATCTTTTTCGCTAGACTGTAATAGGAACAACACGAGATTA 300
QY 792 ATCTGATTTGTTACTCAGAAAGCTTTGATGACAGTGTGATTTTCTTCCGGAACAAC 851
Db 301 ATCTGATTTGTTACTCAGAAAGCTTTGATGACAGTGTGATTTTCTTCCGGAACAAC 360
QY 852 AACTTATTCAGAAAGCGAAATTTCTGTCATGAGAAAGCTTTCTTCTATCATCTGAA 911
Db 361 AACTTATTCAGAAAGCGAAATTTCTGTCATGAGAAAGCTTTCTTCTATCATCTGAA 420
QY 912 TGGAGCGTTATGACACACTGATGATCTGTCCTCCGACCATGATTCATGAAATA 971
Db 421 TGGAGCGTTATGACACACTGATGATCTGTCCTCCGACCATGATTCATGAAATA 480
QY 972 AAGACACCTAAACCTATTCATATTCGCTTACGCTTTGGGGTGGGGAACCTTAGAGT 1031
Db 481 AAGACACCTAAACCTATTCATATTCGCTTACGCTTTGGGGTGGGGAACCTTAGAGT 540
QY 1032 CTCAGTCAAAAGTGTGGCCCTGTGCTGTTCTGGAGCAGGCTTCTGAGGAGTGTG 1091
Db 541 CTCAGTCAAAAGTGTGGCCCTGTGCTGTTCTGGAGCAGGCTTCTGAGGAGTGTG 600
QY 1092 AGCGTACCTTTACCTCAGAGTGAGATGTCCTCATGATGATCTTTGGAGCTGCTTCCC 1151
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QY 1152 AAGGAATAAATGATGCTGCTGTGTAACAGCAACAGCAAGGCTTTCTTCTGAGCC 1211
Db 661 AAGGAATAAATGATGCTGCTGTGTAACAGCAACAGCAAGGCTTTCTTCTGAGCC 720
QY 1212 TTGAGATATGCTGATTTCTCACTTGGAGATTAAGATTAATTTATCCTATCAGAGACTG 1271
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RESULT 3
AL581997 1201 bp mRNA linear EST 01-JUN-2003
LOCUS AL581997 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DL003YG24 5'-PRIME, mRNA sequence.
ACCESSION AL581997
VERSION AL581997.2 GI:31320228
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT On Feb 16, 2001 this sequence version replaced gi:12949550.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0DL003BD12QP1&cluster=1287.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DL003BD12QP1.

FEATURES
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/clone="CS0DL003YG24"
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/cell_line="RAMOS CELL LINE"
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25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 293 a 286 c 277 g 310 t 35 others
ORIGIN

Query Match 53.3%; Score 827; DB 9; Length 1201;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 827; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 AGTCCCAAGCAGAGTCCGGTTGATGATTCCTGATTCGAAATTCCTCCGTTCTGAT 246
Db 115 AGTCCCAAGCAGAGTCCGGTTGATGATTCCTGATTCGAAATTCCTCCGTTCTGAT 174
QY 247 GGATTTGAAGCTCTCTTCTTCTGCTGAATGACTTTCGATCCCTCTGTTGCTGAGAG 306
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Db 235 TTGGACAAATGTTGATTAAGTGTGAGCAAGGCCACACATACATGTAATACACTTT 294
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Db 295 CCTGACCAATGACTGACTGAGAAAGTGTGAGAGGCTGCAAAAAGAGCAGACT 354
QY 427 CATCTCTCCATCAATCCGCTTATCTCCGACCCATGAAAGGCAATACCTGGACACTG 486
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QY 607 TACCTCCAGGCGCAATACCTCTTCCAAAGCTCCCAACCTACAGAGGGAACCAACG 666
Db 535 TACCTCCAGGCGCAATACCTCTTCCAAAGCTCCCAACCTACAGAGGGAACCAACG 594
QY 667 AGTAGAATTCACGTTAATCAACCAAGACCTGAGCAAAAGTCAATGCTGCAAGTGAAG 726
Db 595 AGTAGAATTCACGTTAATCAACCAAGACCTGAGCAAAAGTCAATGCTGCAAGTGAAG 654
QY 727 AATTGACGCTGTTCTGCTACTCTTTTCTGCTAGACTGTAATGAGAAACAACAG 786
Db 655 AATTGACGCTGTTCTGCTACTCTTTTCTGCTAGACTGTAATGAGAAACAACAG 714
QY 787 GATTAATGTAATGATCTCAAGAGGCTTATGAGAGTGAATTTCTTCCGGAA 846
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RESULT 4	
LOCUS	BX446370
DEFINITION	BX446370 Homo sapiens 1201 bp mRNA linear EST 22-MAY-2003
ACCESSION	BX446370
VERSION	BX446370
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1201) Ll,M.B., Gruber,C., Jesse,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
AUTHORS	Contact: Genoscope
TITLE	Genoscope - Centre National de Sequencage
JOURNAL	BP 191 91006 EVRY cedex - France
COMMENT	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1287.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CLDBA004ZB1RPL&cluster=1287.f . Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue genoscope sequence ID : CLDBA004ZB1RPL.
FEATURES	
source	Location/Qualifiers 1..1201

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/clone="CLOBA0044B11"
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/notes="vector: pcwmSPORT_6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcwmSPORT 6 vector.
Library was not normalized."

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Query Match	52.0%	Score 808	DB 13	Length 1201
Best Local Similarity	99.9%	Pred. No. 0		
Matches	858	Conservative	0	Mismatches
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				Gaps
				0
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QY	449	ATCTTCGACCCCATGAAGCGCATTAACCTCGGAACACATGGAAGAGAGCGCTGGTGAATCCGG	508	
Db	130	ATCTTCGACCCCATGAAGCGCATTAACCTCGGAACACATGGAAGAGAGCGCTGGTGAATCCGG	189	
QY	509	GCTCTGGAGAACAGAGTCGCTATCTACTCTCCATATACAGCCTATGATGCTGGCCCCAG	568	
Db	190	GCTCTGGAGAACAGAGTCGCTATCTACTCTCCATATACAGCCTATGATGCTGGCCCCAG	249	
QY	569	GGCGTCAACAACACTGGTTGGCTAAAGGGGCTTGGAGCTTGTACCTCCAGGCCCATATACACTCT	628	
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QY	629	TCCAAAGCTCCCAACTACCCCTACAGAGAGGAAACACCGAGTAGAATTCAACGTTAACTAC	688	
Db	310	TCCAAAGCTCCCAACTACCCCTACAGAGAGGAAACACCGAGTAGAATTCAACGTTAACTAC	369	
QY	689	ACCCAAAGACCTGGACCAAAGTCATGTCTGCACTGAAAGGAATGACGGTGTCTGTCTACT	748	
Db	370	ACCCAAAGACCTGGACCAAAGTCATGTCTGCACTGAAAGGAATGACGGTGTCTGTCTACT	429	
QY	749	TCTTTTTCCTGCTAGAGACTGCTAATGAGGAACAACACGGATTAATCTGAATTGACTCAG	808	

Db	430	TCCTTTTCGTGTAGACGTCGTAAATGAGGAACAAACACGAGATTATCTGAATTGTACTACAG	489
OY	809	AAGCCTTTGATGCAAGGTGTGATTTTCTTTCCCGGAACAACAACCTTTATCAGAAACGC	868
Db	490	AAGCCTTTGATGCAAGGTGTGATTTTCTTTCCCGGAACAACAACCTTTATCAGAAACGC	549
OY	869	GAAATTCGTACACGAGAAACCTTTGGCTTCTACATACCTGGAATGGGACGGTTATGCACA	928
Db	550	GAAATTCGTACACGAGAAACCTTTGGCTTCTACATACCTGGAATGGGACGGTTATGCACA	609
OY	929	CTGATGTAATCTGTCTCCCTGGCAACCATGATTTGATCGAATTAATAAGACACCTAAACTA	988
Dc	610	CTGATGTAATCTGTCTCCCTGGCAACCATGATTTGATCGAATTAATAAGACACCTAAACTA	669
OY	989	TCTCATATTCGCTTAGCCCTTGGGGTGGGGGAACCTTAGAGTCTCAAGTAAAGTGGTG	1048
Db	670	TCTCATATTCGCTTAGCCCTTGGGGTGGGGGAACCTTAGAGTCTCAAGTAAAGTGGTG	729
OY	1049	GCCCTGTGTGGTGTCTGGGAGAGAGCTTTGCAAGGGTGTGAGAGCTTGACCTTTACCTC	1108
Db	730	GCCCTGTGTGTGGTGTCTGGGAGAGAGCTTTGCAAGGGTGTGAGAGCTTGACCTTTACCTC	789
OY	1109	ACAGGTGAGATGTCCCATCATGATTACTTTGGATGCTGCTTCCCAAGGAATTAATGTCAATC	1168
Db	790	ACAGGTGAGATGTCCCATCATGATTACTTTGGATGCTGCTTCCCAAGGAATTAATGTCAATC	849
OY	1169	CTCTGTGAAACACAGCAACACTGAAACGAGCTTTCTTTTGACCTTCCAGATATGCTGGAT	1228
Db	850	CTCTGTGAAACACAGCAACACTGAAACGAGCTTTCTTTTGACCTTCCAGATATGCTGGAT	909
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RESULT 5
AL521920
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL521920 957 bp mRNA linear EST 22-MAY-2003
AL521920 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
cDNA clone CS0DB003XP14 5-PRIME, mRNA sequence.
AL521920
AL521920.2 GI:31040194
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 957)
Li,W.B., Gruber,C., Jesssee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb.13, 2001 this sequence version replaced gi:12785413.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1287.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0DB003DH07QPL&cluster=1287.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DB003DH07QPL.
Location/Qualifiers
1..957
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/clone="CS0DB003XP14"
/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"

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QY		668	GTAGAATTTCACAAGTTAATCTACACCAAGACCTGGACAAAAGTCATGTCTGCAGTGAAGA	727
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QY		848	AAACAACCTTATATCAAGAAAGCGGAAATTTCTGTCACTGGAGAAAGCCTTTCCTTCAATACT	907
Dd		691	AAACAACCTTATATCAAGAAAGCGGAAATTTCTGTCACTGGAGAAAGCCTTTCCTTCAATACT	750
QY		908	GGAATGGAGACGCTATGACACACTGAGTAAGTAATCTGTCCCGGGAACCATGATATGATGCA	967
Dd		751	GGAATGGAGACGCTATGACACACTGAGTAAGTAATCTGTCCCGGGAACCATGATATGATGCA	810
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Dd		811	ATAAA 814	
RESULT 7		BQ229243		
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VERSION		BQ229243.1		
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		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		NIH-MGC http://mgc.ncl.nih.gov/.		
AUTHORS		National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE		Unpublished		
JOURNAL		Contact: Robert Strausberg, Ph.D.		
COMMENT		Email: cga@bs-remail.nih.gov		
		Tissue Procurement: ATCC/DCTP/DRP		
		CDNA Library Preparation: Life Technologies, Inc.		
		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
		DNA Sequencing by: Agencourt Bioscience Corporation		
		Clone distribution: MGC clone distribution information can be		
		found through the I.M.A.G.E. Consortium/LNL at:		
		http://image.lnl.gov		
		Plate: LRAM13315 row: f column: 01		
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		/tissue="melanotic melanoma"		
		/lab_host="DH10B (phage-resistant)"		
		/clone_id="NIH_MGC_72"		
		/note="Organ: skin; Vector: pCMV-Sport6; Site:1: NotI;		
		Site:2: SalI; Cloned unidirectionally. Primer: oligo dt.		
		Average insert size 2 kb. Library constructed by Life		
		Technologies."		
BASE COUNT		218 a 203 c 200 g 211 t 2 others		
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	Best Local Similarity	100.0%;	Pred. No. 0;			
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QY	250	TTTGAAGGCTTCCTCTTCCTTCCTTGAATGACCTTTCATCCCTCTCGCTTGTCTGAGATTG	309			
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QY	370	GACCAATGACCTGACTGAGAAAGTATGAGAGAGGTGCTGCAAAAAGAGCAGACTCAT	429			
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QY	430	TCTCTCTACCATCCGCTATCTTCGCAACCATGAAGGCGATTAACCTGGAACATGGAA	489			
Db	181	TCTCTCTACCATCCGCTATCTTCGCAACCATGAAGGCGATTAACCTGGAACATGGAA	240			
QY	490	GGACGCGCTGTGTATCCGGGCTCGAGAAACAGATGGATATCTACTCTCTCATACAGC	549			
Db	241	GGACGCGCTGTGTATCCGGGCTCGAGAAACAGATGGATATCTACTCTCTCATACAGC	300			
QY	550	CTATGATGCTGCGCCGCCAGGGCGTCAACACTGTGTTGGCTAAAGGGCTTGGAGCTTGAC	609			
Db	301	CTATGATGCTGCGCCGCCAGGGCGTCAACACTGTGTTGGCTAAAGGGCTTGGAGCTTGAC	360			
QY	610	CTCCAGGCGCATPATATCCTTCCAAAGCCCAACATACCTCAGAGGGGAACCAACCGAGT	669			
Db	361	CTCCAGGCGCATPATATCCTTCCAAAGCCCAACATACCTCAGAGGGGAACCAACCGAGT	420			
QY	670	AGAAATCAACCTTACTACACCAACAGACTTGACAAAGTCAATGTCAGTGAAGAGAT	729			
Db	421	AGAAATCAACCTTACTACACCAACAGACTTGACAAAGTCAATGTCAGTGAAGAGAT	480			
QY	730	TGACGGGTGTTCTGTCACTTCTTTTTCGTCTAGACCTGTGTAATGAGAAACAACAGGAT	789			
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QY	790	TAACTGAATGTACTCAGAAAGCGTTGGATCAGGTGGTAGATTTCTTTCCCGGAACAA	849			
Db	541	TAACTGAATGTACTCAGAAAGCGTTGGATCAGGTGGTAGATTTCTTTCCCGGAACAA	600			
QY	850	ACAACCTTATAGAAAGACGAAATTCGTCTACTGGAAGAGCCTTGCTTCTACATACGG	909			
Db	601	ACAACCTTATAGAAAGACGAAATTCGTCTACTGGAAGAGCCTTGCTTCTACATACGG	660			
QY	910	AATGGAGCGTTATGACACACTGATGATCTGTCTCCCTGGCAACCATGATGATCGAAT	969			
Db	661	AATGGAGCGTTATGACACACTGATGATCTGTCTCCCTGGCAACCATGATGATCGAAT	720			
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LOCUS						
DEFINITION	AL529615 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens					
ACCESSION	CDNA clone CSDD0067H18 5-PRIME, mRNA sequence.					
VERSION	AL529615					
KEYWORDS	AL529615.2 GI:31067458					
SOURCE	EST.					
ORGANISM	Homo sapiens (human)					
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1. M. B., Gruber, C., Jesse, J. and Polayes, D.					
AUTHORS	Full-length cDNA libraries and normalization					
TITLE	Unpublished					
JOURNAL						

COMMENT On Feb 13, 2001 this sequence version replaced gi:12793108.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1287.f For more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DD006DD09Qf1cluster=1287.f. Contact :
 Peng Liang Email : liang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DD006DD09Qf1.
 Location/Qualifiers
 1. 1201

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 /clone_id="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
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 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 319 a 286 c 274 g 299 t 23 others
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Query Match 49.1%; Score 763; DB 9; Length 1201;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 913; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 129 CGGTTTGTATATCCCGATCTGCAATTCCTCCGTTCTTCATGATTTGAAGGCTC 188
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 Qy 263 CTTTCTCTCTGAATGATTCGATCCCTCTCGTTCTGAGATTTGGACAAATGTTGA 322
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 Db 489 CCCAGAGGCTCAACAACATGTTGGCTTAAGGGCTTGAGCTTACCTCAGGCCATA 548
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 Db 549 CATCTCTTCAAAAGCTCCCACTACCTACAGAGAGAAACACAGTAGAATTAACGTT 608
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RESULT 9 929 bp mRNA linear EST 16-OCT-2002
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 LOCUS
 DEFINITION AGENCOURT_10422791 NIH_MGC_109 Homo sapiens cDNA clone
 IMAGE:6650148 5', mRNA sequence.
 ACCESSION B0859307
 VERSION B0859307.1 GI:24044299.
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 929)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMU at:
 http://image.llnl.gov
 Plate: L1CM2894 row: 0 column: 12
 High quality sequence stop: 754.
 Location/Qualifiers
 1. 929

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 /clone="IMAGE:6650148"
 /tissue_type="teratocarcinoma, cell line"
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 /clone_id="NIH_MGC_109"
 /note="Organ: ovary; Vector: pOT87; Site:1: EcoRI; Site:2:
 XhoI; cDNA made by oligo-dT priming. directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
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BASE COUNT 251 a 212 c 218 g 247 t 1 others
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 Best Local Similarity 99.8%; Pred. No. 0;

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QY	611	TCAGGCGCATACATCCCTTCCAAAGCTCCCACTACCTTACAGAGGAAACCCAGTA	670						
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QY	671	GATTCACAGTTAACTACACACAGCTGAGCAAGTATGCTCAGTGAAGGAAT	730						
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QY	1211	CTTCGAGATATGCTGATCTCTCACTTGAAGATTAATTAATCTATCAGAGCT	1270						
Db	721	CTTCGAGATATGCTGATCTCTCACTTGAAGATTAATTAATCTATCAGAGCT	780						
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DEFINITION	AGEK000T_6563433 NIH_MGC_88 Homo sapiens cDNA IMAGE:5739935								
ACCESSION	BM557530								
VERSION	BM557530.1	GI:18799594							
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SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
	1 (bases 1 to 1019)								
	NIH-MGC http://mhc.ncl.nih.gov/ .								

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLNL2754 row: a column: 24 High quality sequence stop: 685. Location/Qualifiers 1..1019
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BASE COUNT	256 a 254 c 236 g 271 t 2 others
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Query Match	46.5%; Score 722; DB 12; Length 1019;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 722; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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QY	247 GGAATTAAGAGCT
Db	109 GGAATTAAGAGCT
QY	307 TTGGGCAATGTTGGATTACTGTGTGAACACCCACACATCTGTAAATACACTT
Db	169 TTGGGCAATGTTGGATTACTGTGTGAACACCCACACATCTGTAAATACACTT
QY	367 CCGGACCAATGACCTGAGAGAGTGTGAGAGGTGCTCAAAAGAGCAGACCT
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QY	487 GAAGGAGCGCTGTGTATCCGGCTCTGGGAACAAGTCGGATCTACTCTCTATAC
Db	349 GAAGGAGCGCTGTGTATCCGGCTCTGGGAACAAGTCGGATCTACTCTCTATAC
QY	547 AGCCTATGATGCTGCCCGCAGGCGCTCAACAACCTGTTGGCTAAAGGCTTG
Db	409 AGCCTATGATGCTGCCCGCAGGCGCTCAACAACCTGTTGGCTAAAGGCTTG
QY	607 TACCTCAGGCGCATACATCTTCCCAAGCTCCCACTACCTCAGAGGAAACACCG
Db	469 TACCTCAGGCGCATACATCTTCCCAAGCTCCCACTACCTCAGAGGAAACACCG
QY	667 AGTGAATTCACGTTAACTACACCCCAACACCTGGCAAGATCTCTGCAAGTAA
Db	529 AGTGAATTCACGTTAACTACACCCCAACACCTGGCAAGATCTCTGCAAGTAA
QY	727 AATTGAGGCTGTTCTGCTCACTCTTTCTGCTAGAGCTGTAATGAGAAACACAG
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/clone="IMAGE:334609"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone.lib="NIH_MGC_20"
/Note="Organ: skin; Vector: pOT7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(C). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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48 TTGTAGATTCCTGATCTGCATATCTTCCCGTTCCTTCATGATTTGAAGGCTCTCTT 107

267 CTTCCTGATGATCTTTCATCCCTCTCTGTTGCTGAGAGTTGGACATGTTGATAC 326
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108 CTTCCTGATGATCTTTCATCCCTCTCTGTTGCTGAGAGTTGGACATGTTGATAC 167

327 TGGTGAACCAAGCCACACATACATCTGTAATACATCTCTGACCAATGACCTACAG 386
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168 TGGTGAACCAAGCCACACATACATCTGTAATACATCTCTGACCAATGACCTACAG 227

387 AGGAAGTATGAGAGAGTGTCTGCAAAAGAGGAGACCTATCTCTCTACCATCCG 446
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228 AGGAAGTATGAGAGAGTGTCTGCAAAAGAGGAGACCTATCTCTCTACCATCCG 287

447 CATCTTCGACCCATGAGAGCGCATACCTGGAACATAGGAAGCGCTGCTATCC 506
|||||
288 CATCTTCGACCCATGAGAGCGCATACCTGGAACATAGGAAGCGCTGCTATCC 347

507 GGGCTCTGGAGAGACAGATCGGTATCTACTCTCCATACAGCCTATGATGCTGCGCC 566
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348 GGGCTCTGGAGAGACAGATCGGTATCTACTCTCCATACAGCCTATGATGCTGCGCC 407

567 AGGGCTCAACAACCTGTTGGCTAAAGGCTTGGAGCTTGTACTCCAGGCCATACATC 626
|||||
408 AGGGCTCAACAACCTGTTGGCTAAAGGCTTGGAGCTTGTACTCCAGGCCATACATC 467

627 CTTCGAAGCTCCCACTACCTACAGAGAGGAACACGAGTAGAATTCAACGTTAACT 686
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468 CTTCGAAGCTCCCACTACCTACAGAGAGGAACACGAGTAGAATTCAACGTTAACT 527

687 ACAACCAAGACCTGACAAAGTATCTGCACTGAAAGGAATTGACGCTGTTCTGCA 746
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528 ACAACCAAGACCTGACAAAGTATCTGCACTGAAAGGAATTGACGCTGTTCTGCA 587

747 CTTCCTTTCTGCTAGAGCTGTTAATGAGAACAAACAGGATTAACTGAAATTGACTC 806
|||||
588 CTTCCTTTCTGCTAGAGCTGTTAATGAGAACAAACAGGATTAACTGAAATTGACTC 647

807 AGAAGCTTTGATGACAGTGTGATGATTTCTTCCCGGAACAACACTTATCAGAGA 866
|||||
648 AGAAGCTTTGATGACAGTGTGATGATTTCTTCCCGGAACAACACTTATCAGAGA 707

867 CGGAATTCGTGACTG 883
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708 CGGAATTCGTGACTG 724

RESULT 13
B0526538 919 bp mRNA linear EST 13-SEP-2002
LOCUS B0526538
DEFINITION AGENCOURT_10181989 NIH_MGC_101 Homo sapiens cDNA clone
IMAGE:6536226 5', mRNA sequence.

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ACCESSION B0526538
VERSION B0526538.1 GI:22836979
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 919)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2697 row: d column: 18
High quality sequence stop: 696.
Location/Qualifiers
1..919
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6536226"
/issue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone.lib="NIH_MGC_101"
/Note="Organ: lung; Vector: pOT7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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BASE COUNT 230 a 226 c 229 g 228 t 6 others

Query Match 43.5%; Score 675; DB 13; Length 919;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGATTTATCTTGTGCTGACAGAGACAGCAAGAGAGATTTGGTCAGAAAAGTGC 60
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24 GTGATTTATCTTGTGCTGCTGACAGAGACAGCAAGAGAGATTTGGTCAGAAAAGTGC 83

61 CTTGCCGACACAGACAGCGCATGATGAGGACAGGGCTCTGACTCAGACTTAACGCG 120
|||||
84 CTTGCCGACACAGACAGCGCATGATGAGGACAGGGCTCTGACTCAGACTTAACGCG 143

121 CTGTGCTGCTGCTTTTCTCTCTGTTGAAAAAGGCTGAAAGTGGCACTGAATGAGCA 180
|||||
144 CTGTGCTGCTGCTTTTCTCTCTGTTGAAAAAGGCTGAAAGTGGCACTGAATGAGCA 203

181 TAGATGATCCGACGACAGTCCGTTTGTAGATTCCTGATGCAATCTCCCGTTC 240
|||||
204 TAGATGATCCGACGACAGTCCGTTTGTAGATTCCTGATGCAATCTCCCGTTC 263

241 CTTCATGATTTGAAGGCTCTCTTCTCTCTGATGATGATGATGATGATGATGATGATG 300
|||||
264 CTTCATGATTTGAAGGCTCTCTTCTCTCTGATGATGATGATGATGATGATGATGATG 323

301 TGAGAGTTGGGACATGTTGATTTACTGTTGAGAACCAAGCCACACATCTGTAATAC 360
|||||
324 TGAGAGTTGGGACATGTTGATTTACTGTTGAGAACCAAGCCACACATCTGTAATAC 383

361 ACTCTTCCTGACCAATGACTGACTGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAG 420
|||||
384 ACTCTTCCTGACCAATGACTGACTGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAG 443

QY 421 AGACCTATCTCTCTACCATCCGCTATCTTCGACCCATGAAGCGCATACCTGGAA 480
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Db 444 AGACCTATCTCTCTACCATCCGCTATCTTCGACCCATGAAGCGCATACCTGGAA 503
QY 481 CACATGGAAGAGGCGCTGTGTATCCGGCTCTGGAGAACAGATCGGTATCTACTCTCC 540
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Db 504 CACATGGAAGAGGCGCTGTGTATCCGGCTCTGGAGAACAGATCGGTATCTACTCTCC 563
QY 541 TCATACAGCTATATATCTGCGCCCGCAGGCGCTCAACAACCTGTTGGCTAAAGGCGTTGG 600
|||||
Db 564 TCATACAGCTATATATCTGCGCCCGCAGGCGCTCAACAACCTGTTGGCTAAAGGCGTTGG 623
QY 601 AGCTTACCTCCAGGCGCATACATCTCTCCAAAGCTCCCAACCTACCTTCAGAGGGAAA 660
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Db 624 AGCTTACCTCCAGGCGCATACATCTCTCCAAAGCTCCCAACCTACCTTCAGAGGGAAA 683
QY 661 CCACCGAGTAGAATT 675
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Db 684 CCACCGAGTAGAATT 698

RESULT 14
BQ437698 877 bp mRNA linear EST 24-MAY-2002
LOCUS AGENCOURT.7894666 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6158334
DEFINITION 5', mRNA sequence.

ACCESSION BQ437698
VERSION BQ437698.1 GI:21176774
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 877)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCID/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM13505 row: k column: 07
High quality sequence stop: 667.
Location/Qualifiers

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6158334"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 247 a 181 c 206 g 242 t 1 others
ORIGIN

Query Match 43.4%; Score 674; DB 13; Length 877;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 CAGAGGGAACACCGAGTAGAATTCAAGTAACTACACCAAGAGCTGACAAAGTCA 710
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Db 24 CAGAGGGAACACCGAGTAGAATTCAAGTAACTACACCAAGAGCTGACAAAGTCA 83

QY 711 TGTCGAGTGAAGAAATGACGGTGTTCCTGTCACCTCTTTTCTGCTAGGACTGTA 770
|||||
Db 84 TGTCGAGTGAAGAAATGACGGTGTTCCTGTCACCTCTTTTCTGCTAGGACTGTA 143
QY 771 ATGAGGAACAAACACGGATTATCTGAATTGTACTCAGAAAGCTTTGATGAGGTGTAG 830
|||||
Db 144 ATGAGGAACAAACACGGATTATCTGAATTGTACTCAGAAAGCTTTGATGAGGTGTAG 203
QY 831 ATTTCCTTCCCGGACAAACTTATTCAGAAAGAGGGAATCTGTCATGAGAAAC 890
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Db 204 ATTTCTCTTCCCGGACAAACTTATTCAGAAAGAGGGAATCTGTCATGAGAAAC 263
QY 891 CTTCGCTCTACATCTGATGATGAGAGCGATTATGACACTGATGAATCTGTCCTCGG 950
|||||
Db 264 CTTCGCTCTACATCTGATGATGAGAGCGATTATGACACTGATGAATCTGTCCTCGG 323
QY 951 CAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1010
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Db 324 CAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 383
QY 1011 GGTGGGGAACACCTTAGAGTCTCAAGTCAAGTCTGAGGCGCTGTGCTGTGGGA 1070
|||||
Db 384 GGTGGGGAACACCTTAGAGTCTCAAGTCAAGTCTGAGGCGCTGTGCTGTGGGA 443
QY 1071 GCAGCGTCTGACAGGCTGTGAGGCTGACCTTACCTGACAGTGAAGTGTCCATCATG 1130
|||||

Db 444 GCAGCGTCTGACAGGCTGTGAGGCTGACCTTACCTGACAGTGAAGTGTCCATCATG 503
QY 1131 ATACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1190
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Db 504 ATACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 563
QY 1191 AACGAGGCTTCTTCTGACCTTGAAGTATGCTGAGTCTGACACTTGGAGAAATGATA 1250
|||||

Db 564 AACGAGGCTTCTTCTGACCTTGAAGTATGCTGAGTCTGACACTTGGAGAAATGATA 623
QY 1251 ATATTATTCCTATCAGAGACTGACAGGAGCCCTTTCAGAGTGTATATTCAGAGAAATC 1310
|||||
Db 624 ATATTATTCCTATCAGAGACTGACAGGAGCCCTTTCAGAGTGTATATTCAGAGAAATC 683
QY 1311 AGATTAACACATTC 1324
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Db 684 AGATTAACACATTC 697

RESULT 15
BE797115 963 bp mRNA linear EST 20-SEP-2000
LOCUS 601587094F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941518 5',
DEFINITION mRNA sequence.

ACCESSION BE797115
VERSION BE797115.1 GI:10218313
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 963)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCID/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at: image.llnl.gov
Plate: LLM793 row: k column: 23
High quality sequence stop: 756.
Location/Qualifiers

FEATURES
source 1..963

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/organism="Homo sapiens"  
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/db_xref="taxon:9606"  
/clone="IMAGE:3941518"  
/tissue_type="small cell carcinoma"  
/cell_line="MGC3"  
/lab_host="DH10B (phage-resistant)"  
/clone_lib="NH_MGC_7"  
/note="Organ: lung; Vector: POT87; Site_1: XhoI; Site_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGG(C). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT      239 a      254 c      226 g      244 t  
ORIGIN
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Query Match      42.0%; Score 652; DB 10; Length 963;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY      202 CCGGTTGTAGATTCCTGATCGCAATCTCCCGTCTCTCATGATTTGAAGCTCT 261  
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Db      1 CCGGTTGTAGATTCCTGATCGCAATCTCCCGTCTCTCATGATTTGAAGCTCT 60  
  
QY      262 CCTTCTTCCTTGAATGACTTTCATCCCTCTCGTTTGTGAGAGTTGGACAATGTTGG 321  
      |||  
Db      61 CCTTCTTCCTTGAATGACTTTCATCCCTCTCGTTTGTGAGAGTTGGACAATGTTGG 120  
  
QY      322 ATTACTGTGGAACCAAGCCACACATACCTGTAATATACACTCTTCCGACCAATGACCT 381  
      |||  
Db      121 ATTACTGTGGAACCAAGCCACACATACCTGTAATATACACTCTTCCGACCAATGACCT 180  
  
QY      382 GACTGAGGAATGATGAGAGAGTGTCTGCAAAAAGAGGACGACCTATTCTCTCTACCA 441  
      |||  
Db      181 GACTGAGGAATGATGAGAGAGTGTCTGCAAAAAGAGGACGACCTATTCTCTCTACCA 240  
  
QY      442 TCCGCTATCTTCGACCCATGAAAGCATTAACCTGAAACATGGAAGAGGCGCTGTG 501  
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Db      241 TCCGCTATCTTCGACCCATGAAAGCATTAACCTGAAACATGGAAGAGGCGCTGTG 300  
  
QY      502 GATCCGGGCTCTGGAGAACAGAGTCGATCTACTCTCTCATACAGCCATGATGCTGC 561  
      |||  
Db      301 GATCCGGGCTCTGGAGAACAGAGTCGATCTACTCTCTCATACAGCCATGATGCTGC 360  
  
QY      562 GCCCGAGGGGCTCAAACTGCTTGAAGGCTTGAAGCTTGTACTCCAGGCCCAT 621  
      |||  
Db      361 GCCCGAGGGGCTCAAACTGCTTGAAGGCTTGAAGCTTGTACTCCAGGCCCAT 420  
  
QY      622 ACATCCTTCCAAAGCTCCCAACTACCTACAGAGGAAACACCGAGTAGAATTCAACGT 681  
      |||  
Db      421 ACATCCTTCCAAAGCTCCCAACTACCTACAGAGGAAACACCGAGTAGAATTCAACGT 480  
  
QY      682 TAACTACACCAAGACCTGGAACAAGTCATGTCGACGTGAAGAATGACGGTGTTC 741  
      |||  
Db      481 TAACTACACCAAGACCTGGAACAAGTCATGTCGACGTGAAGAATGACGGTGTTC 540  
  
QY      742 TGTCACTTCTTTTCTGCTAGGACTGTAATAGGAACAACACGATTAATCTGAATTG 801  
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Db      541 TGTCACTTCTTTTCTGCTAGGACTGTAATAGGAACAACACGATTAATCTGAATTG 600  
  
QY      802 TACTCAGAGGCTTTGATCAGGTGTAGATTCTTTCCCGGACAAACAA 853  
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Db      601 TACTCAGAGGCTTTGATCAGGTGTAGATTCTTTCCCGGACAAACAA 652
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Job time : 2396 secs